

>gi|15126197|gb|AAE73433.1| Sequence 2 from patent US 6242217
gi|21517369|gb|AAM60707.1| Sequence 83 from patent US 6399761
Length = 411

Score = 783 bits (2023), Expect = 0.0
Identities = 410/411 (99%), Positives = 411/411 (100%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII 60
MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT 120
GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT
Sbjct: 61 GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT 120

Query: 121 SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
Sbjct: 121 SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGI AKVEDTFIKWNVSQTKIRIISTII FILFGCVLFVALPAIIFKHIEGWSALD 240
LGTIFGKGI AKVEDTFIKWNVSQTKIRIISTII FILFGCVLFVALPAIIFKHIEGWSALD
Sbjct: 181 LGTIFGKGI AKVEDTFIKWNVSQTKIRIISTII FILFGCVLFVALPAIIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLD FYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLD FYKPVVFWILVGLAYFAAVLSMIGDWLRVIS
Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLD FYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHNQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHNQ
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTL SVNHLTNERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK 411
ELTPCRRTL SVNHLT+ERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK
Sbjct: 361 ELTPCRRTL SVNHLT SERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK 411

>gi|15126199|gb|AAE73435.1| Sequence 6 from patent US 6242217
Length = 411

Score = 764 bits (1974), Expect = 0.0
Identities = 394/411 (95%), Positives = 406/411 (98%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD TTINVMKWKT VSTIFLVVLYLII 60
MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKT VSTIFLVVLYLII
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKT VSTIFLVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGI IPLGNT 120
GA VFKALEQP EISQRTTIVI QKQTFI+QH+CVNSTELDELIQQIVAAINAGI IPLGN+
Sbjct: 61 GAAVFKALEQPQEISQRTTIVI QKQTFIAQHACVNSTELDELIQQIVAAINAGI IPLGNS 120

Query: 121 SNQISHWDLGSSFF FAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

SNQ+SHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
 Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

 Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIFKHIEGWSALD 240
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

 Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

 Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ
 Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

 Query: 361 ELTPCRRTLSVNHLTNERDVLPLLLKTESIYLNGLTPHCAGEEIAVIENIK 411
 ELTPC RTLSVNHLT+ER+VLPLLLK ESIYLNGLTPHCAGE+IAVIEN+K
 Sbjct: 361 ELTPCMRTLSVNHLTSEREVLPLLLKAESIYLNGLTPHCAGEDIAVIENMK 411

>gi|10042828|emb|CAC07711.1| unnamed protein product [Mus sp.]
 Length = 370

Score = 684 bits (1766), Expect = 0.0
 Identities = 356/368 (96%), Positives = 364/368 (98%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDITINVMKWKTVSTIFLVVLYLII 60
 MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVLYLII
 Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

 Query: 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120
 GA VFKALEQP EISQRTTIVIQKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNT+
 Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

 Query: 121 SNQISHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
 SNQ+SHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
 Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

 Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIFKHIEGWSALD 240
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

 Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

 Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ
 Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

 Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

>gi|17917944|gb|AAE85378.1| Sequence 8 from patent US 6309855

Length = 370

Score = 681 bits (1758), Expect = 0.0

Identities = 355/368 (96%), Positives = 363/368 (98%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLII 60
 MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVVLII

Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII 60

Query: 61 GATVFKALEQPHEISQRTTIVIQQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120
 GA VFKALEQP EISQRTTIVIQQTFI+QH+CVNSTELDELIQQIVAAINAGIIPGN+

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQISHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
 SNQ+SHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPL GFLLAGVGDQ

Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD

Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ

Sbjct: 301 KKTKEEVGEFRAHAAEWANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRT 368
 ELTPC RT

Sbjct: 361 ELTPCMRT 368

INSTANT
SEQ ID NO: 4

gi|15126199|gb|AAE73435.1| Sequence 6 from patent US 6242217
Length = 411

Score = 784 bits (2025), Expect = 0.0
Identities = 410/411 (99%), Positives = 410/411 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII 60
MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD
Sbjct: 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS
Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK 411
ELTPC RTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK
Sbjct: 361 ELTPCMRTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK 411

>gi|15126197|gb|AAE73433.1| Sequence 2 from patent US 6242217
gi|21517369|gb|AAM60707.1| Sequence 83 from patent US 6399761
Length = 411

Score = 768 bits (1984), Expect = 0.0
Identities = 396/411 (96%), Positives = 407/411 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII 60
MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVVLII
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESD+TTINVMKWKTVSTIFLVVVLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
GA VFKALEQP EISQRTTIVIQKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNT
Sbjct: 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQQIVAAINAGIIPLGNT 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

SNQ+SHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
Sbjct: 121 SNQISHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD
Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS
Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTLSVNHLTSEREVLPPLLKAESIYNGLTPHCAGEDIAVIENMK 411
ELTPCRRTLSVNHLTSE+VLPPLLK ESIYNGLTPHCAGE+IAVIEN+K
Sbjct: 361 ELTPCRRTLSVNHLTSE+VLPPLLKTESIYNGLTPHCAGEEIAVIENIK 411

>gi|10042828|emb|CAC07711.1| unnamed protein product [Mus sp.]
Length = 370

Score = 696 bits (1797), Expect = 0.0
Identities = 367/368 (99%), Positives = 367/368 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII 60
MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII
Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQVSHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
Sbjct: 121 SNQVSHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD
Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS
Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

>gi|17917944|gb|AAE85378.1| Sequence 8 from patent US 6309855

Length = 370

Score = 693 bits (1789), Expect = 0.0

Identities = 366/368 (99%), Positives = 366/368 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII

Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPL GFLLAGVGDQ

Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD

Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ

Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

DIFFERENT FROM SEQ ID NO:4 at residue 366:

L5 ANSWER 2 OF 3 DGENE COPYRIGHT 2003 THOMSON DERWENT on STN
ACCESSION NUMBER: AAY28497 Protein DGENE
TITLE: New two pore potassium channel used for, e.g.
treatment of

cancer, pulmonary, cardiovascular and inflammatory
diseases

INVENTOR: Chapman C G; Meadows H J
PATENT ASSIGNEE: (SMIK) SMITHKLINE BEECHAM PLC.
PATENT INFO: WO 9937762 A1 19990729
APPLICATION INFO: WO 1998-EP7805 19981202
PRIORITY INFO: GB 1998-22135 19981009
EP 1998-300570 19980127

44p

DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1999-469126 [39]
CROSS REFERENCES: N-PSDB: AAZ00040
DESCRIPTION: Mouse h-TREK1 polypeptide.

AN AAY28497 Protein DGENE

AA 37 A; 14 R; 14 N; 14 D; 0 B; 5 C; 14 Q; 23 E; 0 Z; 28 G; 7 H;
42 I;

39 L; 23 K; 5 M; 25 F; 14 P; 29 S; 27 T; 8 W; 9 Y; 34 V; 0

Others

SQL 411

SEQ

1 maapdlldpk saaqnskpri sfsskptvla srvesdsain vmkwktvsti
51 flvvvlylii gaavfkaleq pqueisqrtdi viqkqtfiaq hacvnsteld

=====

101 eliqqivaai nagiipngs snqvshwdlg ssffaggtvi ttigfgnisp
151 rteggkifci iyallgipfl gfltagvgdq lgtifgkgia kvedtfikwn
201 vsqtkiriis tiifilfgcv lfvalpavif khiegwsald aiyyfvitlt
251 tigfgdyvag gsdieyldfy kpvvfwilv glayfaavls migdwlrvls
301 kktkeevgef rahaaewtan vtaefketrr rlsveiydkf qratsvkrkl
351 saelagnhnq eltpcmrtls vnhltserev lppllkaesi ylngltphca
401 gediavienm k

HITS AT: 65-76

1 maapdlldpk saaqnskpri sfsskptvla srvesdsain vmkwktvsti
51 flvvvlylii gaavfkaleq pqueisqrtdi viqkqtfiaq hacvnsteld
101 eliqqivaai nagiipngs snqvshwdlg ssffaggtvi ttigfgnisp
151 rteggkifci iyallgipfl gfltagvgdq lgtifgkgia kvedtfikwn
201 vsqtkiriis tiifilfgcv lfvalpavif khiegwsald aiyyfvitlt
251 tigfgdyvag gsdieyldfy kpvvfwilv glayfaavls migdwlrvls
301 kktkeevgef rahaaewtan vtaefketrr rlsveiydkf qratsvkrkl
351 saelagnhnq eltpcmrtls vnhltserev lppllkaesi ylngltphca
401 gediavienm k

L11 ANSWER 23 OF 33 PCTFULL COPYRIGHT 2003 Univentio on STN
 ACCESSION NUMBER: 2001046258 PCTFULL ED 20020827
 TITLE (ENGLISH): TRANSPORTERS AND ION CHANNELS
 TITLE (FRENCH): TRANSPORTEURS ET CANAUX IONIQUES
 INVENTOR(S): BAUGHN, Mariah, R.;

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 YANG, Junming;
 REDDY, Roopa;
 LAL, Preeti;
 HILLMAN, Jennifer, L.;
 AZIMZAI, Yalda;
 YUE, Henry;
 NGUYEN, Danniel, B.;
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 GANDHI, Ameena, R.;
 TANG, Y., Tom;
 KHAN, Farrah, A.

PATENT ASSIGNEE(S): INCYTE GENOMICS, INC.;
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 REDDY, Roopa;
 LAL, Preeti;
 HILLMAN, Jennifer, L.;
 AZIMZAI, Yalda;
 YUE, Henry;
 NGUYEN, Danniel, B.;
 YAO, Monique, G.;
 GANDHI, Ameena, R.;
 TANG, Y., Tom;
 KHAN, Farrah, A.

DOCUMENT TYPE:
 PATENT INFORMATION:

NUMBER	KIND	DATE
WO 2001046258	A2	20010628

DESIGNATED STATES
 W:

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
 CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
 IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
 MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM
 TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD
 SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
 DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF
 CG CI CM GA GN GW ML MR NE SN TD TG

APPLICATION INFO.:
 PRIORITY INFO.:

WO 2000-US35095	A	20001222
US 1999-60/172,000		19991223
US 2000-60/176,083		20000114
US 2000-60/177,332		20000121
US 2000-60/178,572		20000128
US 2000-60/179,758		20000202
US 2000-60/181,625		20000210

L6 ANSWER 4 OF 4 MEDLINE on STN DUPLICATE 2
 ACCESSION NUMBER: 1999254548 MEDLINE
 DOCUMENT NUMBER: 99254548 PubMed ID: 10321245
 TITLE: Inhalational anesthetics activate two-pore-domain
 background K⁺ channels.
 AUTHOR: Patel A J; Honore E; Lesage F; Fink M; Romey G; Lazdunski M
 CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et
 Cellulaire-CNRS-UPR 411, Valbonne, France.
 SOURCE: NATURE NEUROSCIENCE, (1999 May) 2 (5) 422-6.
 Journal code: 9809671. ISSN: 1097-6256.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199905
 ENTRY DATE: Entered STN: 19990607
 Last Updated on STN: 19990607
 Entered Medline: 19990525
 AB Volatile anesthetics produce safe, reversible unconsciousness, amnesia and
 analgesia via hyperpolarization of mammalian neurons. In molluscan
 pacemaker neurons, they activate an inhibitory synaptic K⁺ current (IKAn),
 proposed to be important in general **anesthesia**. Here we show
 that TASK and **TREK-1**, two recently cloned mammalian
 two-P-domain K⁺ channels similar to IKAn in biophysical properties, are
 activated by volatile general anesthetics. Chloroform, diethyl ether,
 halothane and isoflurane activated **TREK-1**, whereas
 only halothane and isoflurane activated TASK. Carboxy (C)-terminal
 regions were critical for anesthetic activation in both channels. Thus
 both **TREK-1** and TASK are possibly important target
 sites for these agents.

L17 ANSWER 16 OF 84 MEDLINE

ACCESSION NUMBER: 95355355 MEDLINE

DOCUMENT NUMBER: 95355355 PubMed ID: 7629068

TITLE: Amino terminus and the first four membrane-spanning segments of the Arabidopsis K⁺ channel KAT1 confer inward-rectification property of plant-animal chimeric channels.

AUTHOR: Cao Y; Crawford N M; Schroeder J I

CORPORATE SOURCE: Department of Biology, University of California at San Diego, La Jolla 92093-0116, USA.

CONTRACT NUMBER: GM40672 (NIGMS)

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Jul 28) 270 (30) 17697-701.

Journal code: HIV; 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199509

ENTRY DATE: Entered STN: 19950921

Last Updated on STN: 19990129

Entered Medline: 19950905

AB The Arabidopsis hyperpolarization-activated (inward-rectifying) K⁺ **channel** KAT1 is structurally more similar to animal depolarization-activated (**outward**-rectifying) K⁺ **channels** than to animal hyperpolarization-activated K⁺ **channels**. To gain insight into the structural basis for the opposite voltage dependences of plant inward-rectifying and animal **outward**-rectifying K⁺ **channels**, we constructed recombinant chimeric **channels** between the hyperpolarization-activated K⁺ **channel** KAT1 and a Xenopus depolarization-activated K⁺ **channel**. We report here that two of the chimeric constructs, which contain the first third of the KAT1 sequence, including the first four membrane-spanning segments

(S1-S4)

and the linker sequence between the fourth and fifth membrane-spanning segments, express functional channels that retain activation by hyperpolarization, but not depolarization. These two chimeric **channels** are no longer selective for K⁺. The chimeras are selective for cations over anions and are permeable to Ca²⁺. Therefore, unlike animal hyperpolarization-activated K⁺ **channels**, in which the carboxyl terminus is important for inward rectification induced by Mg²⁺ and polyamine block, the plant KAT1 channel has its major determinants for inward rectification in the amino-terminal region, which ends at the end of the S4-S5 linker.

WEST**End of Result Set**

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11/15/96

L1: Entry 2 of 2

File: USPT

Jan 11, 2000

US-PAT-NO: 6013470

DOCUMENT-IDENTIFIER: US 6013470 A

TITLE: Family of mammalian potassium channels, their cloning and their use especially for the screening of drugs

DATE-ISSUED: January 11, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lesage; Florian	Nice			FR
Guillemare; Eric	Nice			FR
Fink; Michel	Cannes La Bocca			FR
Duprat; Fabrice	Valluris			FR
Lazdunski; Michel	Nice			FR
Romey; Georges	Nice			FR
Barhanin; Jacques	Nice			FR

US-CL-CURRENT: 435/69.1; 435/320.1, 435/325, 536/23.1

CLAIMS:

We claim:

1. An isolated and purified nucleic acid molecule encoding a mammalian protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
2. An isolated and purified nucleic acid molecule encoding a human protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
3. The nucleic acid molecule of claim 2 encoding a human protein which exhibits weak inward rectification.
4. The nucleic acid molecule of claim 3 which is expressed in brain and heart tissue and in addition, in at least one of the following tissues: placenta, liver, skeletal, muscle, kidney and pancreas.
5. The human nucleic acid sequence of claim 2 which comprises the sequence represented by SEQ ID No. 1. *encodes SEQ ID NO. 5*
6. A self replication vector comprising the nucleic acid molecule of claim 2.
7. A cell transformed with the self replicating vector of claim 6, which cell expresses a human protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
8. A micro-injected cell comprising the RNA transcript synthesized from the nucleic acid molecule of claim 2, which cell expresses a human protein which

comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.

9. The transformed cell of claim 7, which cell is selected from the group consisting of prokaryotes and eukaryotes.

10. The transformed cell of claim 9 which is a bacterium.

11. The transformed cell of claim 10 which is a yeast, insect, plant or mammalian cell.

12. A method for the production of a human protein competent to transport potassium across a membrane which comprises 2 P domains and 4 transmembrane segments, comprising transferring the vector of claim 6 into a cellular host, culturing the cellular host under conditions allowing the production of said potassium channel, and purifying the human potassium channel.

13. The method of claim 12 wherein the cellular host is selected from the group consisting of prokaryotes and eukaryotes.

14. A pharmaceutical composition for the compensation of a deficiency in potassium channels at the level of one or more tissues, which comprises an isolated and purified nucleic acid molecule encoding a human protein comprising 2 P domains and 4 transmembrane segments which protein is competent to transport potassium across a membrane.

15. A pharmaceutical composition which comprises human cells transformed with the nucleic acid molecule of claim 2.

WEST**End of Result Set**☐

Generate Collection

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L4: Entry 1 of 1

File: USPT

Jan 11, 2000

DOCUMENT-IDENTIFIER: US 6013470 A

TITLE: Family of mammalian potassium channels, their cloning and their use especially for the screening of drugs

US Patent No. (1):6013470Brief Summary Text (5):

The subunits of the voltage-dependent K^{sup.} channels activated by depolarization (Kv families) and the calcium-dependent K^{sup.} channels exhibit six hydrophobic transmembranal domains, one of which (S4) contains repeated positive charges which confer on these channels their sensitivity to voltage and, consequently, in their functional outward rectification (Logothetis, D. E. et al., 1992, Neuron, 8, 531-540; Bezanilla, F. and Stefani, E., 1994, Annu. Rev. Biophys. Biomol. Struct., 23, 819-846).